

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/508,849

DATE: 03/02/2001
TIME: 13:18:50

Input Set : A:\1110-0266P.ST25.txt
Output Set: N:\CRF3\03022001\I508849.raw

#7
ENTERED

3 <110> APPLICANT: NAGATA, Shigekazu et al.
5 <120> TITLE OF INVENTION: Novel Fas Ligand Derivative
7 <130> FILE REFERENCE: 1110-0266P
9 <140> CURRENT APPLICATION NUMBER: 09/508,849
10 <141> CURRENT FILING DATE: 2000-03-17
12 <150> PRIOR APPLICATION NUMBER: JP P1997-252541
13 <151> PRIOR FILING DATE: 1997-09-17
15 <160> NUMBER OF SEQ ID NOS: 16
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 258
21 <212> TYPE: PRT
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Description of Artificial Sequence: amino acids at
26 111-133 from N terminal are deleted from natural
27 human Fas ligand
29 <400> SEQUENCE: 1
30 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
31 1 3 5 10 15
33 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
34 20 25 30
36 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro
37 35 40 45
39 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Leu Pro
40 50 55 60
42 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
43 65 70 75 80
45 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
46 85 90 95
48 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Pro Ser
49 100 105 110
51 Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly
52 115 120 125
54 Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly
55 130 135 140
57 Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile
58 145 150 155 160
60 Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly
61 165 170 175
63 Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn
64 180 185 190
66 Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser
67 195 200 205
69 Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala
70 210 215 220
72 Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu

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73 225                230                235                240
75 Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr
76                245                250                255
78 Lys Leu
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 277
84 <212> TYPE: PRT
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: Description of Artificial Sequence:amino acids at
89     128-131 from N terminal are deleted from natural
90     human Fas ligang
92 <400> SEQUENCE: 2
93 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
94   1                5                10                15
96 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
97                20                25                30
99 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
100                35                40                45
102 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro
103                50                55                60
105 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
106   65                70                75                80
108 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
109                85                90                95
111 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
112                100                105                110
114 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Gly
115                115                120                125
117 His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His
118                130                135                140
120 Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp
121 145                150                155                160
123 Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly
124                165                170                175
126 Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr
127                180                185                190
129 Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr
130                195                200                205
132 Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys
133                210                215                220
135 Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr
136 225                230                235                240
138 Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn
139                245                250                255
141 Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe
142                260                265                270
144 Gly Leu Tyr Lys Leu
145                275

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148 <210> SEQ ID NO: 3
149 <211> LENGTH: 281
150 <212> TYPE: PRT
151 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <223> OTHER INFORMATION: Description of Artificial Sequence: point mutation
155     of a substitution of Lys 129 for Ala from N
156     terminal is present in natural human Fas ligand
157
159 <400> SEQUENCE: 3
160 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp
161   1             5             10             15
163 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
164           20           25           30
166 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
167       35       40       45
169 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
170   50       55       60
172 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
173 65       70       75       80
175 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
176       85       90       95
178 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
179       100      105      110
181 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
182       115      120      125
184 Ala Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg
185       130      135      140
187 Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu
188 145      150      155      160
190 Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr
191       165      170      175
193 Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
194       180      185      190
196 Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser
197       195      200      205
199 His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met
200       210      215      220
202 Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
203 225      230      235      240
205 Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His
206       245      250      255
208 Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser
209       260      265      270
211 Gln Thr Phe Phe Gly Leu Tyr Lys Leu
212       275      280
215 <210> SEQ ID NO: 4
216 <211> LENGTH: 774
217 <212> TYPE: DNA

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218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
222     amino acids SEQ ID No.1
224 <400> SEQUENCE: 4
225 atgcagcagc ccttcaatta cccatatccc cagatctact gggtaggacag cagtgccagc 60
226 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
227 ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
228 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaaacca cagcacaggc 240
229 ctgtgtctcc ttgtgatgtt ttcatgggtt ctggttgccct tggtaggatt gggcctgggg 300
230 atgtttcagc tcttccacct acagaaggag ccagttccac cccctgaaaa aaaggagctg 360
231 aggaaagtgg ccattttaac aggcaagtcc aactcaaggt ccatgcctct ggaatgggaa 420
232 gacacctatg gaattgtcct gctttctgga gtgaagtata agaagggtgg ccttgtgatc 480
233 aatgaaactg ggctgtactt tgtatatccc aaagtatact tccggggtca atcttgcaac 540
234 aacctgcccc tgagccacaa ggtctacatg aggaactcta agtatcccca ggatctgggtg 600
235 atgatggagg ggaagatgat gagctactgc actactgggc agatgtgggc ccgcagcagc 660
236 tacctggggg cagtgttcaa tcttaccagt gctgatcatt tatatgtcaa cgtatctgag 720
237 ctctctctgg tcaattttga ggaatctcag acgtttttcg gcttatataa gctc      774
240 <210> SEQ ID NO: 5
241 <211> LENGTH: 831
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
247     amino acids SEQ ID No.2
249 <400> SEQUENCE: 5
250 atgcagcagc ccttcaatta cccatatccc cagatctact gggtaggacag cagtgccagc 60
251 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
252 ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
253 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gagggaaacca cagcacaggc 240
254 ctgtgtctcc ttgtgatgtt ttcatgggtt ctggttgccct tggtaggatt gggcctgggg 300
255 atgtttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
256 atgcacacag catcatcttt gggccacccc agtccacccc ctgaaaaaaaa ggagctgagg 420
257 aaagtggccc atttaacagg caagtccaac tcaaggtcca tgcctctgga atgggaagac 480
258 acctatggaa ttgtcctgct ttctggagtg aagtataaga agggtagcct tgtgatcaat 540
259 gaaactgggc tgtactttgt atattccaaa gtatacttcc ggggtcaatc ttgcaacaac 600
260 ctgcccctga gccacaaggt ctacatgagg aactctaagt atccccagga tctgggtgatg 660
261 atggagggga agatgatgag ctactgcact actgggcaga tgtgggcccg cagcagctac 720
262 ctgggggcag tgttcaatct taccagtgtc gatcatttat atgtcaacgt atctgagctc 780
263 tctctggtca attttgagga atctcagacg tttttcggtt tatataagct c      831
266 <210> SEQ ID NO: 6
267 <211> LENGTH: 843
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Description of Artificial Sequence:DNA coding for
273     amino acids SEQ ID No.3
275 <400> SEQUENCE: 6
276 atgcagcagc ccttcaatta cccatatccc cagatctact gggtaggacag cagtgccagc 60

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277 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120
278 ggtcaaagga ggccaccacc accaccgcca ccgccaccac taccacctcc gccgccgccg 180
279 ccaccactgc ctccactacc gctgccaccc ctgaagaaga gaggaacca cagcacaggc 240
280 ctgtgtctcc ttgtgatgtt ttcatgggtt ctggttgctt tggtaggatt ggcctgggg 300
281 atgtttcagc tcttccacct acagaaggag ctggcagaac tccgagagtc taccagccag 360
282 atgcacacag catcatcttt ggaggcaca ataggccacc ccagtccacc ccctgaaaaa 420
283 aaggagctga ggaaagtggc ccatttaaca ggcaagtcca actcaaggtc catgcctctg 480
284 gaatgggaag acacctatgg aattgtctg ctttctggag tgaagtataa gaagggtggc 540
285 ctgtgatca atgaaactgg gctgtacttt gtatattcca aagtatactt ccggggtcaa 600
286 tcttgcaaca acctgcccct gagccacaag gtctacatga ggaactctaa gtatccccag 660
287 gatctggtga tgatggagg gaagatgatg agctactgca ctactgggca gatgtgggc 720
288 cgcagcagct acctgggggc agtgttcaat cttaccagt ctgatcattt atatgtcaac 780
289 gtatctgagc tctctctggt caattttgag gaatctcaga cgtttttcgg cttatataag 840
290 ctc
293 <210> SEQ ID NO: 7
294 <211> LENGTH: 20
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Description of Artificial Sequence:a sense primer
300 BOS6
302 <400> SEQUENCE: 7
303 cctcagacag tggttcaaag 20
306 <210> SEQ ID NO: 8
307 <211> LENGTH: 39
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence:an antisense
313 deletion primer DA4
315 <400> SEQUENCE: 8
316 ttttcagggg gtggactggg ctcttctgt aggtggaag 39
319 <210> SEQ ID NO: 9
320 <211> LENGTH: 28
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Description of Artificial Sequence:HFLP3
327 <400> SEQUENCE: 9
328 gctctagaac attctcggtg cctgtaac 28
331 <210> SEQ ID NO: 10
332 <211> LENGTH: 30
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence:DA5
339 <400> SEQUENCE: 10
340 tggactgggg tggcccaaag atgatgctgt 30
343 <210> SEQ ID NO: 11

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VERIFICATION SUMMARY DATE: 03/02/2001
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